

IN THE CLAIMS:

1. (Currently Amended) A method for producing ergosta-5,7-dienol comprising culturing yeast organisms which have

a reduced Δ22-desaturase activity consisting of the enzymatic activity of Δ22-desaturase having SEQ ID.NO: 2 and

an increased HMG-CoA-reductase activity consisting of the enzymatic activity of HMG-CoA-reductase having SEQ ID.NO: 4 and

an increased squalene epoxidase activity consisting of the enzymatic activity of squalene expoxidase having SEQ ID.NO: 8
in comparison with the wild type organism.

2. (Previously presented) The method as claimed in claim 1, wherein, in order to reduce the Δ22-desaturase activity, the gene expression of a nucleic acid encoding a Δ22-desaturase is reduced in comparison with the wild type organism.

3. (Previously presented) The method as claimed in claim 2, wherein an organism without a functional Δ22-desaturase gene is used.

4. (Previously presented) The method as claimed in claim 1, wherein, in order to increase the HMG-CoA reductase activity, the gene expression of a nucleic acid encoding an HMG-CoA reductase is increased in comparison with the wild type organism.

5. (Previously presented) The method as claimed in claim 4, wherein, in order to increase gene expression, a nucleic acid construct comprising a nucleic acid encoding an HMG-CoA reductase is introduced into the organism and whose expression in the organism is subject to reduced regulation in comparison with the wild type organism.

6. (Previously presented) The method as claimed in claim 5, wherein the nucleic acid

construct comprises a promoter which, in the organism, is subject to reduced regulation in comparison with the wild-type promoter.

7. (Previously presented) The method as claimed in claim 6, wherein the nucleic acid encoding an HMG-CoA reductase is a nucleic acid whose expression in the organism is subject to reduced regulation in comparison with the homologous, orthologous nucleic acid.

8. (Previously presented) The method as claimed in claim 7, wherein the nucleic acid encoding an HMG-CoA reductase is a nucleic acid which encodes the catalytic region of HMG-CoA reductase.

9. (Previously presented) The method as claimed in claim 8, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 4.

10. (Previously presented) The method as claimed in claim 9, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 3 is introduced.

11. (Withdrawn) The method as claimed in any claim 1, wherein, in order to increase the lanosterol C 14-demethylase activity, the gene expression of a nucleic acid encoding a lanosterol C14-demethylase is increased in comparison with the wild type.

12. (Withdrawn) The method as claimed in claim 11, wherein, in order to increase gene expression, one or more nucleic acids encoding a lanosterol C14-demethylase are introduced into the organism.

13. (Withdrawn) The method as claimed in claim 12, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 6 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids

which has at least 30% identity with the sequence SEQ. ID. NO. 6 at the amino acid level, which proteins have the enzymatic characteristic of a lanosterol C14-demethylase.

14. (Withdrawn) The method as claimed in claim 13, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 5 is introduced.

15. (Previously presented) The method as claimed in claim 1, wherein, in order to increase the squalene epoxidase activity, the gene expression of a nucleic acid encoding a squalene epoxidase is increased in comparison with the wild type organism.

16. (Previously presented) The method as claimed in claim 15, wherein, in order to increase gene expression, one or more nucleic acids encoding a squalene epoxidase are introduced into the organism.

17. (Previously presented) The method as claimed in claim 16, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 8.

18. (Previously presented) The method as claimed in claim 17, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 7 is introduced.

19. (Withdrawn) The method as claimed in claim 1, wherein, in order to increase the squalene synthetase activity, the gene expression of a nucleic acid encoding a squalene synthetase is increased in comparison with the wild type.

20. (Withdrawn) The method as claimed in claim 19, wherein, in order to increase gene expression, one or more nucleic acids encoding a squalene synthetase are introduced into the organism.

21. (Withdrawn) The method as claimed in claim 20, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 10 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 30% identity with the sequence SEQ. ID. NO. 10 at the amino acid level, which proteins have the enzymatic characteristic of a squalene synthetase.

22. (Withdrawn) The method as claimed in claim 21, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 9 is introduced.

23. (Cancelled)

24. (Previously presented) The method as claimed in claim 1, wherein, after the cultivation, the organism is harvested and ergosta-5,7-dienol is subsequently isolated from the organism.

25. (Withdrawn) A genetically modified organism, where the genetic modification reduces the Δ22-desaturase activity and increases the HMG-CoA reductase activity and increases at least one of the activities selected from the group consisting of lanosterol C 14-demethylase activity, squalene epoxidase activity and squalene synthetase activity in comparison with the wild type.

26. (Withdrawn) The genetically modified organism as claimed in claim 25, where the genetic modification reduces the Δ22-desaturase activity and increases the HMG-CoA reductase activity and increases the lanosterol C 14-demethylase activity in comparison with the wild type.

27. (Withdrawn) The genetically modified organism as claimed in claim 25, wherein the genetically modified organism has an increased content in ergosta-5,7-dienol and/or its biosynthetic intermediates and/or metabolites in comparison with the wild type.

28. (Withdrawn) The genetically modified organism as claimed in claim 25, wherein the organism used is yeast.

29. (Currently Amended) A method for the production of ergosta-5, 7-dienol comprising culturing a genetically modified yeast organism, wherein the genetic modification

reduces the $\Delta 22$ -desaturase activity consisting of the enzymatic activity of $\Delta 22$ -desaturase having SEQ ID.NO: 2 and

increases the HMG-CoA reductase activity consisting of the enzymatic activity of HMG-CoA reductase having SEQ ID.NO: 4 and

increases squalene epoxidase activity consisting of the enzymatic activity of squalene epoxidase having SEQ ID.NO: 8

in comparison with the wild type.

30. (Withdrawn) A method for the generation of a genetically modified organism in which, starting from a starting organism,

the $\Delta 22$ -desaturase activity is reduced and

the HMG-CoA reductase activity is increased and

at least one of the activities selected from the group consisting of lanosterol C14-demethylase activity, squalene epoxidase activity and squalene synthetase activity is increased.

31. (Canceled)

32. (Canceled)